

1815

N/A

Gucker

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/977,862

CRF Processing Date: 1/16/98  
Edited by: [signature]  
Verified by: [signature] (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: deleted stray mark under (vii) PRIOR APP. DATA section

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/977,862DATE: 01/21/98  
TIME: 09:56:10

INPUT SET: S22663.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

- 1  
2  
3 (1) General Information  
4  
5 (i) APPLICANT: Lawrence, Geoffrey  
6  
7 (ii) TITLE OF THE INVENTION: Novel Compounds  
8  
9  
10 (iii) NUMBER OF SEQUENCES: 6  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Ratner & Prestia  
14 (B) STREET: P.O. Box 980  
15 (C) CITY: Valley Forge  
16 (D) STATE: PA  
17 (E) COUNTRY: USA  
18 (F) ZIP: 19482  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Diskette  
22 (B) COMPUTER: IBM Compatible  
23 (C) OPERATING SYSTEM: DOS  
24 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
25  
26 (vi) CURRENT APPLICATION DATA:  
--> OK 27 (A) APPLICATION NUMBER: To be assigned  
28 (B) FILING DATE: Herewith  
29 (C) CLASSIFICATION:  
30  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: GB 96 24677.2  
33 (B) FILING DATE: Filed November 27, 1996  
34  
35  
36 (A) APPLICATION NUMBER: GB 9709463.5  
37 (B) FILING DATE: May 9, 1997  
38  
39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: Prestia, Paul F.  
41 (B) REGISTRATION NUMBER: 23,031  
42 (C) REFERENCE/DOCKET NUMBER: GH30170  
43  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: 610-407-0700  
46 (B) TELEFAX: 610-407-0701

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/08/977,862

DATE: 01/21/98  
TIME: 09:56:13

INPUT SET: S22663.raw

47 (C) TELEX: 846169

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 1200 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

57

58 (ii) MOLECULE TYPE: cDNA

59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

61

62	ATGGTGC GCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCGTAG	TCCTGATGTT	GCTGCTGCTG	60
63	CTGCCGCGGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
64	ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGCTGCC	180
65	TACCACCACC	TGGATTCTCT	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
66	TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
67	TGCATGTGCC	ACCGGCGCAT	GAAGAACCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
68	CACCGTGCCC	GCAGCCTTGG	TAACATATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
69	ACCAGCAAAC	CCTGGAAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
70	CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
71	GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
72	CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
73	GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
74	CTGCCGCGCT	TGGCCCCCAA	CTGCCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
75	TGCAGATCAC	GCCTGGTGGA	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
76	TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
77	ACCCCCAACT	TTGTCAAGCA	TGTCAACACC	AGTGTTCGCT	TAAGCTGCAC	CTGCCGAGGC	960
78	AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
79	CTCACGGAGG	CCATTGCAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
80	CCACACCCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
81	CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

82

83 (2) INFORMATION FOR SEQ ID NO:2:

84

85 (i) SEQUENCE CHARACTERISTICS:

86 (A) LENGTH: 400 amino acids

87 (B) TYPE: amino acid

88 (C) STRANDEDNESS: single

89 (D) TOPOLOGY: linear

90

91 (ii) MOLECULE TYPE: peptide

92

93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

94

95	Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
96	1				5					10					15	
97	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
98				20					25					30		
99	Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/977,862

DATE: 01/21/98  
TIME: 09:56:17.

INPUT SET: S22663.raw

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100          35          40          45
101 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
102          50          55          60
103 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
104          65          70          75          80
105 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
106          85          90          95
107 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
108          100          105          110
109 Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
110          115          120          125
111 Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
112          130          135          140
113 Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
114          145          150          155          160
115 Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
116          165          170          175
117 Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
118          180          185          190
119 Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
120          195          200          205
121 Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
122          210          215          220
123 Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
124          225          230          235          240
125 Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
126          245          250          255
127 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
128          260          265          270
129 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
130          275          280          285
131 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
132          290          295          300
133 Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
134          305          310          315          320
135 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
136          325          330          335
137 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
138          340          345          350
139 Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
140          355          360          365
141 Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
142          370          375          380
143 Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
144          385          390          395          400
145
146
147
148
149
150
151
152

```

## (2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/08/977,862

DATE: 01/21/98  
TIME: 09:56:20

INPUT SET: S22663.raw

```

153
154      (ii) MOLECULE TYPE: cDNA
155
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
157
158      ATGGTGC GCC  CCCTGAACCC  GCGACCGCTG  CCGCCCCGTAG  TCCTGATGTT  GCTGCTGCTG      60
159      CTGCCGCCGT  CGCCGCTGCC  TCTCGCAGCC  GGAGACCCCC  TTCCCACAGA  AAGCCGACTC     120
160      ATGAACAGCT  GTCTCCAGGC  CAGGAGGAAG  TGCCAGGCTG  ATCCCACCTG  CAGTGATGCC     180
161      TACCACCACC  TGGATTCCCTG  CACCTCTAGC  ATAAGCACCC  CACTGCCCTC  AGAGGAGCCT     240
162      TCGGTCCCTG  CTGACTGCCT  GGAGGCAGCA  CAGCAACTCA  GGAACAGCTC  TCTGATAGGC     300
163      TGCATGTGCC  ACCGGCGCAT  GAAGAACCAG  GTTGCCCTGCT  TGGACATCTA  TTGGACCGTT     360
164      CACCGTGCCC  GCAGCCTTGG  TAACTATGAG  CTGGATGTCT  CCCCTATGA  AGACACAGTG     420
165      ACCAGCAAAC  CCGGAAAAAT  GAATCTCAGC  AAACCTGAACA  TGCTCAAACC  AGACTCAGAC     480
166      CTCTGCCTCA  AGTTTGCCAT  GCTGTGTA CTCAATGACA  AGTGTGACCG  GCTGCGCAAG     540
167      GCCTACGGGG  AGGCGTGCTC  CGGGCCCCAC  TGCCAGCGCC  ACGTCTGCCT  CAGGCAGCTG     600
168      CTCACTTTCT  TCGAGAAGGC  CGCCGAGCCC  CACGCGCAGG  GCCTGCTACT  GTGCCCATGT     660
169      GCCCCAACG  ACCGGGGCTG  CGGGGAGCGC  CGGCGCAACA  CCATCGCCCC  CAACTGCGCG     720
170      CTGCCGCTG  TGGCCCCCAA  CTGCCTGGAG  CTGCGGCGCC  TCTGCTTCTC  CGACCCGCTT     780
171      TGCAGATCAC  GCCTGGTGGA  TTTCAGACC  CACTGCCATC  CCATGGACAT  CCTAGGAACT     840
172      TGTGCAACAG  AGCAGTCCAG  ATGTCTACGA  GCATACCTGG  GGCTGATTGG  GACTGCCATG     900
173      ACCCCCAACT  TTGTCAGCAA  TGTCAACACC  AGTGTTCCT  TAAGCTGCAC  CTGCCGAGGC     960
174      AGTGGCAACC  TGCAGGAGGA  GTGTGAAATG  CTGGAAGGGT  TCTTCTCCCA  CAACCCCTGC    1020
175      CTCACGGAGG  CCATTGCAGC  TAAGATGCGT  TTTCACAGCC  AACTCTTCTC  CCAGGACTGG    1080
176      CCACACCTTA  CCTTTGCTGT  GATGGCACAC  CAGAATGAAA  ACCCTGCTGT  GAGGCCACAG    1140
177      CCCTGGGTGC  CCTCTCTTTT  CTCCTGCACG  CTTCCCTTGA  TTCTGCTCCT  GAGCCTATGG    1200

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178
179      (2) INFORMATION FOR SEQ ID NO:4:
180

```

```

181      (i) SEQUENCE CHARACTERISTICS:
182          (A) LENGTH: 400 amino acids
183          (B) TYPE: amino acid
184          (C) STRANDEDNESS: single
185          (D) TOPOLOGY: linear

```

```

186
187      (ii) MOLECULE TYPE: peptide
188

```

```

189      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
190

```

```

191      Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
192      1          5          10          15
193      Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
194      20          25          30
195      Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
196      35          40          45
197      Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Asp Ala Tyr His His Leu
198      50          55          60
199      Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
200      65          70          75          80
201      Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
202      85          90          95
203      Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
204      100         105         110
205      Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn

```

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/977,862

DATE: 01/21/98  
TIME: 09:56:24

INPUT SET: S22663.raw

206		115		120		125	
207	Tyr	Glu	Leu	Asp	Val	Ser	Pro
208		130		135		140	
209	Trp	Lys	Met	Asn	Leu	Ser	Lys
210		145		150		155	
211	Leu	Cys	Leu	Lys	Phe	Ala	Met
212				165		170	
213	Arg	Leu	Arg	Lys	Ala	Tyr	Gly
214				180		185	
215	Arg	His	Val	Cys	Leu	Arg	Gln
216				195		200	
217	Glu	Pro	His	Ala	Gln	Gly	Leu
218				210		215	
219	Arg	Gly	Cys	Gly	Glu	Arg	Arg
220				225		230	
221	Leu	Pro	Pro	Val	Ala	Pro	Asn
222				245		250	
223	Ser	Asp	Pro	Leu	Cys	Arg	Ser
224				260		265	
225	His	Pro	Met	Asp	Ile	Leu	Gly
226				275		280	
227	Leu	Arg	Ala	Tyr	Leu	Gly	Leu
228				290		295	
229	Val	Ser	Asn	Val	Asn	Thr	Ser
230				305		310	
231	Ser	Gly	Asn	Leu	Gln	Glu	Glu
232				325		330	
233	His	Asn	Pro	Cys	Leu	Thr	Glu
234				340		345	
235	Ser	Gln	Leu	Phe	Ser	Gln	Asp
236				355		360	
237	Ala	His	Gln	Asn	Glu	Asn	Pro
238				370		375	
239	Ser	Leu	Phe	Ser	Cys	Thr	Leu
240				385		390	
241						395	
242							
243							
244							
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247							
248							
249							
250							
251							
252							
253							
254							
255							
256							
257							
258							

## (2) INFORMATION FOR SEQ ID NO:5:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

254	GAGCGCCGGC	GCAACACCAT	CGCCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
255	CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTTGCA	GATCAGCCTT	GGTGGATTTC	120
256	CAGACCCACT	GCCATCCCAT	GGACATCCTA	GGAACCTGTG	CAACAGAGCA	GTCCAGATGT	180
257	CTACGAGCAT	ACCTGGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTTGT	CAGCAATGTC	240
258	AACACCAGTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGAGTGT	300

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/977,862**

DATE: 01/21/98  
TIME: 09:56:27

**INPUT SET: S22663.raw**

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER:To be assigned

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/977,862DATE: 01/16/98  
TIME: 14:03:57

INPUT SET: S22663.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

1  
2  
3 (1) General Information  
4  
5 (i) APPLICANT: Lawrence, Geoffrey  
6  
7 (ii) TITLE OF THE INVENTION: Novel Compounds  
8  
9  
10 (iii) NUMBER OF SEQUENCES: 6  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Ratner & Prestia  
14 (B) STREET: P.O. Box 980  
15 (C) CITY: Valley Forge  
16 (D) STATE: PA  
17 (E) COUNTRY: USA  
18 (F) ZIP: 19482  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Diskette  
22 (B) COMPUTER: IBM Compatible  
23 (C) OPERATING SYSTEM: DOS  
24 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER: To be assigned  
28 (B) FILING DATE: Herewith  
29 (C) CLASSIFICATION:  
30  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: GB 96 24677.2  
33 (B) FILING DATE: Filed November 27, 1996  
34 and  
35 (A) APPLICATION NUMBER: GB 9709463.5  
36 (B) FILING DATE: May 9, 1997  
37  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Prestia, Paul F.  
40 (B) REGISTRATION NUMBER: 23,031  
41 (C) REFERENCE/DOCKET NUMBER: GH30170  
42  
43 (ix) TELECOMMUNICATION INFORMATION:  
44 (A) TELEPHONE: 610-407-0700  
45 (B) TELEFAX: 610-407-0701  
46 (C) TELEX: 846169

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/977,862

DATE: 01/16/98  
TIME: 14:03:59

INPUT SET: S22663.raw

47

48

49

50

(2) INFORMATION FOR SEQ ID NO:1:

51

(i) SEQUENCE CHARACTERISTICS:

52

(A) LENGTH: 1200 base pairs

53

(B) TYPE: nucleic acid

54

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

56

57

(ii) MOLECULE TYPE: cDNA

58

59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60

61

ATGGTGCGCC CCCTGAACCC GCGACCGCTG CCGCCCGTAG TCCTGATGTT GCTGCTGCTG 60

62

CTGCCGCGGT CGCCGCTGCC TCTCGCAGCC GGAGACCCCC TTCCCACAGA AAGCCGACTC 120

63

ATGAACAGCT GTCTCCAGGC CAGGAGGAAG TGCCAGGCTG ATCCCACCTG CAGTGCTGCC 180

64

TACCACCACC TGGATTCCCTG CACCTCTAGC ATAAGCACCC CACTGCCCTC AGAGGAGCCT 240

65

TCGGTCCCTG CTGACTGCCCT GGAGGCAGCA CAGCAACTCA GGAACAGCTC TCTGATAGGC 300

66

TGCATGTGCC ACCGGCGCAT GAAGAACCAG GTTGCCTGCT TGGACATCTA TTGGACCGTT 360

67

CACCGTGCCC GCAGCCTTGG TAACTATGAG CTGGATGCTT CCCCCTATGA AGACACAGTG 420

68

ACCAGCAAAC CCTGGAAAAT GAATCTCAGC AAATGAACA TGCTCAAACC AGACTCAGAC 480

69

CTCTGCCTCA AGTTTGCCAT GCTGTGTACT CTCAATGACA AGTGTGACCG GCTGCGCAAG 540

70

GCCTACGGGG AGGCGTGCTC CGGGCCCCAC TGCCAGCGCC ACCTCTGCCCT CAGGCAGCTG 600

71

CTCACTTTCT TCGAGAAGGC CGCCGAGCCC CACGCGCAGG GCCTGCTACT GTGCCCATGT 660

72

GCCCCCAACG ACCGGGGCTG CGGGGAGCGC CGGCGCAACA CCATCGCCCC CAACTGCGCG 720

73

CTGCCGCCTG TGGCCCCCAA CTGCCTGGAG CTGCGGCGCC TCTGCTTCTC CGACCCGCTT 780

74

TGCAGATCAC GCCTGGTGGG TTTCCAGACC CACTGCCATC CCATGGACAT CCTAGGAAC 840

75

TGTGCAACAG AGCAGTCCAG ATGTCCTACG GCATACCTGG GGCTGATTGG GACTGCCATG 900

76

ACCCCCAACT TTGTCAGCAA TGTCAACACC AGTGTTCGCT TAAGCTGCAC CTGCCGAGGC 960

77

AGTGGCAACC TGCAGGAGGA GTGTGAAATG CTGGAAGGGT TCTTCTCCCA CAACCCCTGC 1020

78

CTCACGGAGG CCATTGCAGC TAAGATGCGT TTTCACAGCC AACTCTTCTC CCAGGACTGG 1080

79

CCACACCCTA CCTTTGCTGT GATGGCACAC CAGAAATGAAA ACCCTGCTGT GAGGCCACAG 1140

80

CCCTGGGTGC CCTCTCTTTT CTCCTGCACG CTTCCCTTGA TTCTGCTCCT GAGCCTATGG 1200

81

82

(2) INFORMATION FOR SEQ ID NO:2:

83

84

(i) SEQUENCE CHARACTERISTICS:

85

(A) LENGTH: 400 amino acids

86

(B) TYPE: amino acid

87

(C) STRANDEDNESS: single

88

(D) TOPOLOGY: linear

89

90

(ii) MOLECULE TYPE: peptide

91

92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

93

94

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met

95

1 5 10 15

96

Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp

97

20 25 30

98

Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg

99

35 40 45

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/977,862

DATE: 01/16/98  
TIME: 14:04:02

INPUT SET: S22663.raw

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100 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
101 50 55 60
102 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
103 65 70 75 80
104 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
105 85 90 95
106 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
107 100 105 110
108 Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
109 115 120 125
110 Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
111 130 135 140
112 Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
113 145 150 155 160
114 Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
115 165 170 175
116 Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
117 180 185 190
118 Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
119 195 200 205
120 Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
121 210 215 220
122 Arg Gly Cys Gly Glu Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
123 225 230 235 240
124 Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
125 245 250 255
126 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
127 260 265 270
128 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
129 275 280 285
130 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
131 290 295 300
132 Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
133 305 310 315 320
134 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
135 325 330 335
136 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
137 340 345 350
138 Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
139 355 360 365
140 Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
141 370 375 380
142 Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
143 385 390 395 400

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/977,862DATE: 01/16/98  
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153 (ii) MOLECULE TYPE: cDNA

154

155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

156

157	ATGGTGC GCC	CCCTGAACCC	GCGACCGCTG	CCGCCCCTAG	TCCTGATGTT	GCTGCTGCTG	60
158	CTGCCGCCGT	CGCCGCTGCC	TCTCGCAGCC	GGAGACCCCC	TTCCCACAGA	AAGCCGACTC	120
159	ATGAACAGCT	GTCTCCAGGC	CAGGAGGAAG	TGCCAGGCTG	ATCCCACCTG	CAGTGATGCC	180
160	TACCACCACC	TGGATTCTCT	CACCTCTAGC	ATAAGCACCC	CACTGCCCTC	AGAGGAGCCT	240
161	TCGGTCCCTG	CTGACTGCCT	GGAGGCAGCA	CAGCAACTCA	GGAACAGCTC	TCTGATAGGC	300
162	TGCATGTGCC	ACCGGCGCAT	GAAGAACCAG	GTTGCCTGCT	TGGACATCTA	TTGGACCGTT	360
163	CACCGTGCCC	GCAGCCTTGG	TAACCTATGAG	CTGGATGTCT	CCCCCTATGA	AGACACAGTG	420
164	ACCAGCAAAC	CCTGGAAAAT	GAATCTCAGC	AAACTGAACA	TGCTCAAACC	AGACTCAGAC	480
165	CTCTGCCTCA	AGTTTGCCAT	GCTGTGTACT	CTCAATGACA	AGTGTGACCG	GCTGCGCAAG	540
166	GCCTACGGGG	AGGCGTGCTC	CGGGCCCCAC	TGCCAGCGCC	ACGTCTGCCT	CAGGCAGCTG	600
167	CTCACTTTCT	TCGAGAAGGC	CGCCGAGCCC	CACGCGCAGG	GCCTGCTACT	GTGCCCATGT	660
168	GCCCCCAACG	ACCGGGGCTG	CGGGGAGCGC	CGGCGCAACA	CCATCGCCCC	CAACTGCGCG	720
169	CTGCCGCCTG	TGGCCCCCAA	CTGCCTGGAG	CTGCGGCGCC	TCTGCTTCTC	CGACCCGCTT	780
170	TGCAGATCAC	GCCTGGTGGA	TTTCCAGACC	CACTGCCATC	CCATGGACAT	CCTAGGAACT	840
171	TGTGCAACAG	AGCAGTCCAG	ATGTCTACGA	GCATACCTGG	GGCTGATTGG	GACTGCCATG	900
172	ACCCCCAACT	TTGTCTAGCA	TGTCAACACC	AGTGTTCGCT	TAAGCTGCAC	CTGCCGAGGC	960
173	AGTGGCAACC	TGCAGGAGGA	GTGTGAAATG	CTGGAAGGGT	TCTTCTCCCA	CAACCCCTGC	1020
174	CTCACGGAGG	CCATTGCAGC	TAAGATGCGT	TTTCACAGCC	AACTCTTCTC	CCAGGACTGG	1080
175	CCACACCCTA	CCTTTGCTGT	GATGGCACAC	CAGAATGAAA	ACCCTGCTGT	GAGGCCACAG	1140
176	CCCTGGGTGC	CCTCTCTTTT	CTCCTGCACG	CTTCCCTTGA	TTCTGCTCCT	GAGCCTATGG	1200

177

178 (2) INFORMATION FOR SEQ ID NO:4:

179

180 (i) SEQUENCE CHARACTERISTICS:

181

182 (A) LENGTH: 400 amino acids

183

184 (B) TYPE: amino acid

185

186 (C) STRANDEDNESS: single

187

188 (D) TOPOLOGY: linear

189

190 (ii) MOLECULE TYPE: peptide

191

192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

193

190	Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
191	1				5					10					15	
192	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp	
193				20				25					30			
194	Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
195				35				40					45			
196	Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Asp	Ala	Tyr	His	His	Leu
197		50					55					60				
198	Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
199		65				70				75				80		
200	Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
201				85						90				95		
202	Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
203				100					105					110		
204	Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
205				115				120						125		

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206	Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
207		130					135					140				
208	Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
209		145				150					155				160	
210	Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
211				165						170					175	
212	Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
213				180					185					190		
214	Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
215		195					200					205				
216	Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
217		210					215					220				
218	Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
219		225			230						235				240	
220	Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
221				245					250					255		
222	Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
223				260					265					270		
224	His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
225		275					280					285				
226	Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
227		290				295						300				
228	Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
229		305			310					315					320	
230	Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
231				325					330					335		
232	His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
233				340					345					350		
234	Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
235		355					360					365				
236	Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
237		370					375					380				
238	Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
239		385			390					395					400	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

253	GAGCGCCGGC	GCAACACCAT	CGCCCCCAAC	TGCGCGCTGC	CGCCTGTGGC	CCCCAACTGC	60
254	CTGGAGCTGC	GGCGCCTCTG	CTTCTCCGAC	CCGCTTTGCA	GATCACGCCT	GGTGGATTTC	120
255	CAGACCCACT	GCCATCCCAT	GGACATCCTA	GGAACCTGTG	CAACAGAGCA	GTCCAGATGT	180
256	CTACGAGCAT	ACCTGGGGCT	GATTGGGACT	GCCATGACCC	CCAACTTTGT	CAGCAATGTC	240
257	AACACCACTG	TTGCCTTAAG	CTGCACCTGC	CGAGGCAGTG	GCAACCTGCA	GGAGGAGTGT	300
258	GAAATGCTGG	AAGGGTTCTT	CTCCCACAAC	CCCTGCCTCA	CGGAGGCCAT	TGCAGCTAAG	360

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/977,862**

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Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER:To be assigned